INFORMATION DISCLOSURE STATEMENT	Atty. Docket No.: 6263.N	Serial No.: 09/847,670
	Applicant(s): Finzel et al.	Confirmation No.: 4815
	Filing Date: May 2, 2001	Group: ~~1645~~ 1631

U.S. PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
	CS	6,093,573	07/25/00	Beamer et al.	436	86	

FOREIGN PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Country	Class	Subclass	Translation Yes	Translation No
	CS	WO 93/02209	02/04/93	~~PCT~~ WIPO				
	↓	WO 97/15588	05/01/97	~~PCT~~ WIPO				
	↓	WO 99/36422	07/22/99	~~PCT~~ WIPO				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial		Document Description
	CS	Bartlett et al., "CAVEAT: A Program to Facilitate the Structure-derived Design of Biologically Active Molecules," Molecular Recognition: Chemical and Biological Problems, *Royal Society of Chemistry*, Special Pub. No. 78:182-196 (1989).
		Blundell, T.L. and Johnson, N.L., Protein Crystallography, Academic Press, title page, publication page, and table of contents only (8 pages total) (1976).
		Böhm, "The computer program LUDI: a new method for the de novo design of enzyme inhibitors," *J. Comput. Aided Mol. Des.* 1992;*6*(1):61-78.
		Brünger, "Crystallographic refinement by simulated annealing. Application to a 2.8 Å resolution structure of aspartate aminotransferase," *J. Mol. Biol.* 1988; *203*(3):803-16.
		Brünger, "Extension of molecular replacement: A New search strategy based on Patterson correlation refinement," *Acta Cryst.* 1990; *A46*:46–57.
	↓	Brünger, "Free R value: a novel statistical quantity for assessing the accuracy of crystal structures," *Nature*. 1992;*355*:472-5.

EXAMINER	Date Considered
	7/10/03

*Examiner: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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CS		Brünger, "A system for crystallography and NMR," X-PLOR Manual, Version 3.1, Yale University Press, New Haven, CT (1992) (title page, publication page and table of contents only (13 pages)).
		Cho et al., "Crystal structure of RNA helicase from genotype 1b hepatitis C virus. A feasible mechanism of unwinding duplex RNA," *J. Biol. Chem.* 1998; *273*(24):15045-52.
		Choo et al., "Genetic organization and diversity of the hepatitis C virus," *Proc. Natl. Acad. Sci. U .S. A.* 1991;*88*(6):2451-5.
		Choo et al., "Isolation of a cDNA clone derived from a blood-borne non-A, non-B viral hepatitis genome," *Science*. 1989; *244*:359-62.
		Collaborative Computational Project, No. 4, "The CCP4 suite: programs for protein crystallography" *Acta Cryst.* 1994;*D50*:760-3.
		Eisen et al., "HOOK: a program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," *Proteins: Structure, Function, and Genetics.* 1994;*19*(3):199-221.
		Finzel, "Incorporation of fast Fourier transforms to speed restrained least-squares refinement of protein structures" *J. Appl. Cryst.* 1987;*20*:53-55.
		Gillet et al., "SPROUT: a program for structure generation," *J. Comput. Aided Mol. Des.* 1993;*7*(2):127-53.
		Goodford, "A computational procedure for determining energetically favorable binding sites on biologically important macromolecules," *J. Med. Chem.* 1985; *28*(7):849-57.
		Goodsell et al., "Automated docking of substrates to proteins by simulated annealing," *Proteins: Structure, Function, and Genetics*, 1990;*8*(3):195-202.
		Gorbalenya et al., "Helicases: amino acid sequence comparisons and structure-function relationships,"*Current Opin. in Struct. Biol.* 1993;*3*:419-429.
		Grakoui et al., "Characterization of the hepatitis C virus-encoded serine proteinase: determination of proteinase-dependent polyprotein cleavage sites," *J. Virol.* 1993;*67*(5):2832-43.
		Hendrickson et al., "Incorporation of Sterochemical Information into Crystallographic Refinement" in *Computing in Crystallography*, eds., Diamond et al., Indian Academy of Science, Bangalore, India, pp. 13.01 - 13.25 (1980).

EXAMINER	Date Considered
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		Hendrickson et al., "Selenomethionyl proteins produced for analysis by multiwavelength anomalous diffraction (MAD): a vehicle for direct determination of three-dimensional structure," *EMBO J.* 1990;*9*(5):1665-72.
		Houghton, M., in *Fields virology*, eds., Fields et al., Raven Press, New York, NY, Third Ed., Vol. 1, pp. 1035-1058 (1996).
		Howard et al., "The use of an imaging proportional counter in macromolecular crystallography," *J. Appl. Cryst.* 1987;*20*:383-7.
		Jin et al., "Expression, isolation, and characterization of the hepatitis C virus ATPase/RNA helicase," *Arch. Biochem. Biophys.* 1995;*323*(1):47-53.
		Kabsch, "A discussion of the solution for the best rotation to relate two sets of vectors," *Acta Cryst.* 1978;*A34*:827-8.
		Kang et al., "Crystallization and preliminary X-ray crystallographic analysis of the helicase domain of hepatitis C virus NS3 protein," *Acta Cryst.* 1998; *D54*: 121-3.
		Kim et al., "C-terminal domain of the hepatitis C virus NS3 protein contains an RNA helicase activity," *Biochem. Biophys. Res. Commun.* 1995;*215*(1):160-6.
		Kim et al., "Hepatitis C virus NS3 RNA helicase domain with a bound oligonucleotide: the crystal structure provides insights into the mode of unwinding," *Structure.* 1998;*6*(1):89-100.
		Korolev et al., "Comparisons between the structures of HCV and Rep helicases reveal structural similarities between SF1 and SF2 super-families of helicases," *Protein Sci.* 1998;*7*(3):605-10.
		Kraulis, "MOLSCRIPT: A Program to Produce Both Detailed and Schematic Plots of Protein Structures," *J. Appl. Cryst.* 1991;*24*:946-950.
		Kuntz et al., "A geometric approach to macromolecule-ligand interactions," *J. Mol. Biol.* 1982;*161*(2):269-88.
		Lattman, E., "Diffraction methods for biological macromolecules. Use of the rotation and translation functions," *Methods Enzymol.* 1985;*115*:55-77.
		Lauri et al., "CAVEAT: a program to facilitate the design of organic molecules," *J. Comput. Aided Mol. Des.* 1994;*8*(1):51-66.
		Martin, "3D database searching in drug design," *J. Med. Chem.* 1992; *35*(12):2145-54. Review.

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		Matthews, "Solvent content of protein crystals," *J. Mol. Biol.* 1968;*33*(2):491-7
		Meng et al., "Automated Docking with Grid-Based Energy Evaluation," *J. Comp. Chem.*, 1992;*13*(4):505-524.
		Miranker et al., "Functionality maps of binding sites: a multiple copy simultaneous search method," *Proteins: Structure, Function, and Genetics.* 1991;*11*(1):29-34.
		Navaza, "AMoRe: an automated package for molecular replacement," *Acta Crystallogr.* 1994;*A50*:157-163.
		Nishibata et al., "Automatic Creation of Drug Candidate Structures Based on Receptor Structure. Starting Point for Artificial Lead Generation," *Tetrahedron*, *47*(43):8985-8990 (1991).
		Noren et al., "A general method for site-specific incorporation of unnatural amino acids into proteins," *Science.* 1989;*244*(4901):182-8.
		Pai et al., "Refined crystal structure of the triphosphate conformation of H-ras p21 at 1.35 Å resolution: implications for the mechanism of GTP hydrolysis," *EMBO J.* 1990;*9*(8):2351-9.
		Rossman et al., "The Molecular Replacement Method. A Collection of Papers on the Use of Non-Crystallographic Symmetry," ed., Rossman, M.G., Gordon & Breach, New York, NY, title page, publication page, and table of contents only, 6 pages total (1972).
		Sack, "CHAIN - A Crystallographic Modeling Program," *J Molecular Graphics.* 1988; *6*(4):224-5.
		Steinkühler et al., "Activity of purified hepatitis C virus protease NS3 on peptide substrates," *J. Virol.* 1996;*70*(10):6694-700.
		Tari et al., "Snapshot of an enzyme reaction intermediate in the structure of the ATP-Mg2+-oxalate ternary complex of Escherichia coli PEP carboxykinase," *Nat. Struct. Biol.* 1996;*3*(4):355-63.
		Tatusova et al., "BLAST 2 Sequences, a new tool for comparing protein and nucleotide sequences," *FEMS Microbiol. Lett.* 1999;*174*(2):247-50.
		Tong et al., "The locked rotation function," *Acta Crystallogr.* 1990;*A46*:783-92.

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		Walker et al,. "Distantly related sequences in the alpha- and beta-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold," *EMBO J.* 1982;*1*(8):945-51.
		Wriggers et al, "Protein domain movements: detection of rigid domains and visualization of hinges in comparisons of atomic coordinates," *Proteins: Structure, Function, and Genetics.* 1997;*29*(1):1-14.
		Wyckoff et al., eds., *Methods in Enzymology, Vol. 114 - Diffraction Methods for Biological Macromolecules*, Academic Press, Orlando, FL, title page, publication page, and table of contents only, 5 pages total (1985).
		Wyckoff et al., eds., *Methods in Enzymology, Vol. 115 - Diffraction Methods for Biological Macromolecules*, Academic Press, Orlando, FL, title page, publication page, and table of contents only, 4 pages total (1985).
		Yao et al., "Structure of the hepatitis C virus RNA helicase domain," *Nat. Struct. Biol.* 1997;*4*(6):463-7.

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